3. (Amended) The method of claim 1 [or 2], wherein the polynucleotide sequence encodes a polypeptide or is a control sequence; or wherein the polynucleotide sequence encodes a polypeptide or part thereof and further comprises a control sequence involved in the expression of the polypeptide or a part of such control sequence.

6. (Amended) The method according to [any of] claim[s] 4 [or 5], wherein the enzyme is an aminopeptidase, amylase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase, beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase, invertase, laccase, lipase, mannosidase, mutanase, oxidase, a pectinolytic enzyme, peroxidase, phytase, polyphenoloxidase, a proteolytic enzyme, ribonuclease, transglutaminase, or xylanase.

7. (Amended) The method according to claim 1 [or 2], wherein the control sequence is an enhancer sequence, a leader sequence, a polyadenylation sequence, a propeptide sequence, a promoter, a replication initiation sequence, a signal sequence, a transcriptional terminator or a translational terminator.

9. (Amended) The method according to [any of] claim[s] 1[-8], wherein the selective marker is selected from the group of genes which encode a product which provides for resistance to biocide or viral toxicity, resistance to heavy metal toxicity, or prototrophy to auxotrophs.

12. (Amended) The method of [any of] claim[s] 1 [to 11], wherein the replication initiating sequence is a nucleic acid sequence selected from the group consisting of:

(a) a replication initiating sequence having at least 50% identity with the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2 and is capable of initiating replication;

(b) a replication initiating sequence which hybridises under low stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, or (ii) the

respective complementary strands, wherein the low stringency conditions are defined by prehybridization and hybridization at 42°C in 5x SSPE, 0.3% SDS, 200 mg/ml sheared and denatured salmon sperm DNA, and 25% formamide, and wash conditions are defined at 50°C for 30 minutes in 2x SSC, 0.2% SDS; and

(c) a subsequence of (a) or (b), wherein the subsequence has replication initiating activity.

13. (Amended) The method of claim 12, wherein the nucleic acid sequence has at least 50% identity[, more preferably about 60%, even more preferably about 70%, even more preferably about 80%, even more preferably about 90%, and most preferably about 97% identity] with the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2.

17. (Amended) The method of [any of] claim[s] 12 [to 16], wherein the replication initiating sequence has the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:2, or is a respective functional subsequence thereof.

20. (Amended) The method according to [any of] claim[s]1[-19], wherein the filamentous fungal cell transformed with the population of DNA vectors is a cell of a strain of *Acremonium*, *Aspergillus*, *Coprinus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliopthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium* or *Trichoderma*.

REMARKS

Entry of this amendment is respectfully requested.

Claims 1-28 were initially presented. In this amendment, claims 23-26 are cancelled without prejudice and claims 3, 6, 7, 9, 12, 13, 17, and 20 are amended to correct multiple dependencies. No new matter is added. Accordingly, claims 1-22, 27, and 28 are pending and at issue.